

CALTE.015ASEQLIST.txt

SEQUENCE LISTING

<110> Anderson, David J.
Dong, Xinzhong
Zylka, Mark

<120> IDENTIFICATION OF A RECEPTOR CONTROLLING MIGRATION AND METASTASIS OF SKIN
CANCER CELLS

<130> CALTE.0015A

<150> US 60/391,127

<151> 2000-06-21

<160> 4

<170> FastSEQ for windows Version 4.0

<210> 1

<211> 1361

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (48)...(1064)

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Val Ile Gln Asp Trp Thr Ile Asn Ile Thr Ala Leu Lys Glu Ser Asn		
5 10 15		
gac aat gga ata tca ttt tgt gaa gtt gtg tct cgt acc atg act ttt	152	
Asp Asn Gly Ile Ser Phe Cys Glu Val Val Ser Arg Thr Met Thr Phe		
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ctt tcc ctc atc att gcc tta gtt ggg ctg gtt gga aat gcc aca gtg	200	
Leu Ser Leu Ile Ile Ala Leu Val Gly Leu Val Gly Asn Ala Thr Val		
40 45 50		
tta tgg ttt ctg ggc ttc cag atg agc agg aat gcc ttc tct gtc tac	248	
Leu Trp Phe Leu Gly Phe Gln Met Ser Arg Asn Ala Phe Ser Val Tyr		
55 60 65		
atc ctc aac ctt gct ggt gct gac ttt gtc ttc atg tgc ttt caa att	296	
Ile Leu Asn Leu Ala Gly Ala Asp Phe Val Phe Met Cys Phe Gln Ile		
70 75 80		
gta cat tgt ttt tat att atc tta gac atc tac ttc atc ccc act aat	344	
Val His Cys Phe Tyr Ile Ile Leu Asp Ile Tyr Phe Ile Pro Thr Asn		
85 90 95		
ttt ttt tca tct tac act atg gtg tta aac att gct tac ctt agt ggt	392	
Phe Phe Ser Ser Tyr Thr Met Val Leu Asn Ile Ala Tyr Leu Ser Gly		
100 105 110 115		

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120 125 130	
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135 140 145	
ata tgt act gtg ctt tgg gtc ttg tcc ctg gtg ttg agc ctc ctg gaa Ile Cys Thr Val Leu Trp Val Leu Ser Leu Val Leu Ser Leu Glu	536
150 155 160	
gga aag gaa tgt ggc ttc cta tat tac act agt ggc cct ggt ttg tgt Gly Lys Glu Cys Gly Phe Leu Tyr Tyr Thr Ser Gly Pro Gly Leu Cys	584
165 170 175	
aag aca ttt gat tta atc act act gca tgg tta att gtt tta ttt gtg Lys Thr Phe Asp Leu Ile Thr Thr Ala Trp Leu Ile Val Leu Phe Val	632
180 185 190 195	
gtt ctc ttg gga tcc agt ctg gcc ttg gtg ctt acc atc ttc tgt ggc Val Leu Leu Gly Ser Ser Leu Ala Leu Val Leu Thr Ile Phe Cys Gly	680
200 205 210	
tta cac aag gtt cct gtg acc agg ttg tat gtg acc att gtg ttt aca Leu His Lys Val Pro Val Thr Arg Leu Tyr Val Thr Ile Val Phe Thr	728
215 220 225	
gtg ctt gtc ttc ctg atc ttt ggt ctg ccc tat ggg atc tac tgg ttc Val Leu Val Phe Leu Ile Phe Gly Leu Pro Tyr Gly Ile Tyr Trp Phe	776
230 235 240	
ctc tta gag tgg att agg gaa ttt cat gat aat aaa cct tgt ggt ttt Leu Leu Glu Trp Ile Arg Glu Phe His Asp Asn Lys Pro Cys Gly Phe	824
245 250 255	
cgt aac gtg aca ata ttt ctg tcc tgt att aac agc tgt gcc aac ccc Arg Asn Val Thr Ile Phe Leu Ser Cys Ile Asn Ser Cys Ala Asn Pro	872
260 265 270 275	
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280 285 290	
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295 300 305	
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310 315 320	
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325 330 335	
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gacccaaggt taactcagtt ggggaagtag tcaatgttgt agaagttgat tgatattgaa	1184
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 35 40 45
 Ala Thr Val Leu Trp Phe Leu Gly Phe Gln Met Ser Arg Asn Ala Phe
 50 55 60
 Ser Val Tyr Ile Leu Asn Leu Ala Gly Ala Asp Phe Val Phe Met Cys
 65 70 75 80
 Phe Gln Ile Val His Cys Phe Tyr Ile Ile Leu Asp Ile Tyr Phe Ile
 85 90 95
 Pro Thr Asn Phe Phe Ser Ser Tyr Thr Met Val Leu Asn Ile Ala Tyr
 100 105 110
 Leu Ser Gly Leu Ser Ile Leu Thr Val Ile Ser Thr Glu Arg Phe Leu
 115 120 125
 Ser Val Met Trp Pro Ile Trp Tyr Arg Cys Gln Arg Pro Arg His Thr
 130 135 140
 Ser Ala Val Ile Cys Thr Val Leu Trp Val Leu Ser Leu Val Leu Ser
 145 150 155 160
 Leu Leu Glu Gly Lys Glu Cys Gly Phe Leu Tyr Tyr Thr Ser Gly Pro
 165 170 175
 Gly Leu Cys Lys Thr Phe Asp Leu Ile Thr Thr Ala Trp Leu Ile Val
 180 185 190
 Leu Phe Val Val Leu Leu Gly Ser Ser Leu Ala Leu Val Leu Thr Ile
 195 200 205
 Phe Cys Gly Leu His Lys Val Pro Val Thr Arg Leu Tyr Val Thr Ile
 210 215 220
 Val Phe Thr Val Leu Val Phe Leu Ile Phe Gly Leu Pro Tyr Gly Ile
 225 230 235 240
 Tyr Trp Phe Leu Leu Glu Trp Ile Arg Glu Phe His Asp Asn Lys Pro
 245 250 255
 Cys Gly Phe Arg Asn Val Thr Ile Phe Leu Ser Cys Ile Asn Ser Cys
 260 265 270
 Ala Asn Pro Ile Ile Tyr Phe Leu Val Gly Ser Ile Arg His His Arg
 275 280 285
 Phe Gln Arg Lys Thr Leu Lys Leu Leu Leu Gln Arg Ala Met Gln Asp
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 Ser Pro Glu Glu Glu Glu Cys Gly Glu Met Gly Ser Ser Arg Arg Pro
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 Arg Glu Ile Lys Thr Val Trp Lys Gly Leu Arg Ala Ala Leu Ile Arg
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 gctcaagtct tgtttttgtt tccaggggca ccagtggagg ttttctgagc atg gat 176

Met Asp
1

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Trp Phe Leu Ile Leu Trp Ile Trp Lys Asp Ser Asp Val Leu Phe Cys
245 250 255

cat att cat cca gtt tca gtt gtc ctg tca tct ctt aac agc agt gcc 992
His Ile His Pro Val Ser Val Val Leu Ser Ser Leu Asn Ser Ser Ala
260 265 270

aac ccc atc att tac ttc ttc gtg ggc tct ttt agg aag cag tgg cgg 1040
Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe Arg Lys Gln Trp Arg
275 280 285

ctg cag cag ccg atc ctc aag ctg gct ctc cag agg gct ctg cag gac 1088
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295 300 305

att gct gag gtg gat cac agt gaa gga tgc ttc cgt cag ggc acc ccg 1136
Ile Ala Glu Val Asp His Ser Glu Gly Cys Phe Arg Gln Gly Thr Pro
310 315 320

gag atg tcg aga agc agt ctg gtg tagagatgga cagcctctac ttccatcaga 1190
Glu Met Ser Arg Ser Ser Leu Val
325 330

tatatgtggc tttgagaggc aactttgccc ctgtctgtct gatttgctga actttctcag 1250
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35 40 45
Gly Phe Val Leu Trp Leu Leu Gly Phe Arg Met Arg Arg Asn Ala Phe
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Ser Val Tyr Val Leu Ser Leu Ala Gly Ala Asp Phe Leu Phe Leu Cys
65 70 75 80
Phe Gln Ile Ile Asn Cys Leu Val Tyr Leu Ser Asn Phe Phe Cys Ser
85 90 95
Ile Ser Ile Asn Phe Pro Ser Phe Phe Thr Thr Val Met Thr Cys Ala
100 105 110
Tyr Leu Ala Gly Leu Ser Met Leu Ser Thr Val Ser Thr Glu Arg Cys
115 120 125
Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg Pro Arg His
130 135 140
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145 150 155 160
Ser Ile Leu Glu Gly Lys Phe Cys Gly Phe Leu Phe Ser Asp Gly Asp
165 170 175
Ser Gly Trp Cys Gln Thr Phe Asp Phe Ile Thr Ala Ala Trp Leu Ile
180 185 190
Phe Leu Phe Met Val Leu Cys Gly Ser Ser Leu Ala Leu Leu Val Arg
195 200 205
Ile Leu Cys Gly Ser Arg Gly Leu Pro Leu Thr Arg Leu Tyr Leu Thr
210 215 220
Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu Pro Phe Gly
225 230 235 240

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		275					280					285			
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	290					295					300				
Gln	Asp	Ile	Ala	Glu	Val	Asp	His	Ser	Glu	Gly	Cys	Phe	Arg	Gln	Gly
305					310					315					320
Thr	Pro	Glu	Met	Ser	Arg	Ser	Ser	Leu	Val						
				325					330						